

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/479,862

DATE: 12/20/2000  
TIME: 22:20:58

INPUT SET: S36235.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Takanori OKURA  
6 Kakuji TORIGOE  
7 Masahi KURIMOTO  
8  
9 (ii) TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
10 OF INDUCING THE PRODUCTION OF INTERFERON-  
11  
12 (iii) NUMBER OF SEQUENCES: 35  
13  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: BROWDY AND NEIMARK  
16 (B) STREET: 419 Seventh Street, N.W., Suite 300  
17 (C) CITY: Washington  
18 (D) STATE: D.C.  
19 (E) COUNTRY: USA  
20 (F) ZIP: 20004  
21  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Floppy disk  
24 (B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
26 (D) SOFTWARE: Patent In Release #1.0, Version #1.30  
27  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER: 09/479,862  
30 (B) FILING DATE:  
31 (C) CLASSIFICATION:  
32  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: 08/884,324  
35 (B) FILING DATE:  
36  
37 (viii) ATTORNEY/AGENT INFORMATION:  
38 (A) NAME: BROWDY, Roger L.  
39 (B) REGISTRATION NUMBER: 25,618  
40 (C) REFERENCE/DOCKET NUMBER: OKURA=1  
41  
42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: 202-628-5197  
44 (B) TELEFAX: 202-737-3528  
45  
46 (2) INFORMATION FOR SEQ ID NO: 1:

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47  
48 (i) SEQUENCE CHARACTERISTICS:  
49 (A) LENGTH: 157 amino acids  
50 (B) TYPE: amino acid  
51 (D) TOPOLOGY: linear  
52  
53 (ii) MOLECULE TYPE: peptide  
54  
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
56  
57 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn  
58 1 5 10 15  
59 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
60 20 25 30  
61 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
62 35 40 45  
63 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile  
64 50 55 60  
65 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile  
66 65 70 75 80  
67 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys  
68 85 90 95  
69 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys  
70 100 105 110  
71 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu  
72 115 120 125  
73 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu  
74 130 135 140  
75 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp  
76 145 150 155  
77  
78 (2) INFORMATION FOR SEQ ID NO: 2:  
79  
80 (i) SEQUENCE CHARACTERISTICS:  
81 (A) LENGTH: 1120 base pairs  
82 (B) TYPE: nucleic acid  
83 (C) STRANDEDNESS: double  
84 (D) TOPOLOGY: linear  
85  
86 (ii) MOLECULE TYPE: cDNA to mRNA  
87  
88 (iii) HYPOTHETICAL: No  
89  
90 (iv) ANTI-SENSE: No  
91  
92 (vi) ORIGINAL SOURCE:  
93 (A) ORGANISM: human  
94 (F) TISSUE TYPE: liver  
95  
96 (ix) FEATURE:  
97 (A) NAME/KEY: 5'UTR  
98 (B) LOCATION: 1..177  
99 (C) IDENTIFICATION METHOD: E

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100      (A) NAME/KEY: leader peptide
101      (B) LOCATION: 178..285
102      (C) IDENTIFICATION METHOD: S
103      (A) NAME/KEY: mat peptide
104      (B) LOCATION: 286..756
105      (C) IDENTIFICATION METHOD: S
106      (A) NAME/KEY: 3'UTR
107      (B) LOCATION: 757..1120
108      (C) IDENTIFICATION METHOD: E
109
110      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
111
112      GCCTGGACAG TCAGCAAGGA ATTGTCTCCC AGTGCATTTT GCCCTCCTGG CTGCCAACTC      60
113      TGGCTGCTAA AGCGGCTGCC ACCTGCTGCA GTCTACACAG CTTCGGGAAG AGGAAAGGAA      120
114      CCTCAGACCT TCCAGATCGC TTCCTCTCGC AACAACTAT TTGTCGCAGG AATAAAG      177
115      ATG GCT GCT GAA CCA GTA GAA GAC AAT TGC ATC AAC TTT GTG GCA ATG      225
116      Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
117      -35 -30 -25
118      AAA TTT ATT GAC AAT ACG CTT TAC TTT ATA GCT GAA GAT GAT GAA AAC      273
119      Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
120      -20 -15 -10 -5
121      CTG GAA TCA GAT TAC TTT GGC AAG CTT GAA TCT AAA TTA TCA GTC ATA      321
122      Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
123      1 5 10
124      AGA AAT TTG AAT GAC CAA GTT CTC TTC ATT GAC CAA GGA AAT CGG CCT      369
125      Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
126      15 20 25
127      CTA TTT GAA GAT ATG ACT GAT TCT GAC TGT AGA GAT AAT GCA CCC CGG      417
128      Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
129      30 35 40
130      ACC ATA TTT ATT ATA AGT ATG TAT AAA GAT AGC CAG CCT AGA GGT ATG      465
131      Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
132      45 50 55 60
133      GCT GTA ACT ATC TCT GTG AAG TGT GAG AAA ATT TCA AYT CTC TCC TGT      513
134      Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
135      65 70 75
136      GAG AAC AAA ATT ATT TCC TTT AAG GAA ATG AAT CCT CCT GAT AAC ATC      561
137      Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
138      80 85 90
139      AAG GAT ACA AAA AGT GAC ATC ATA TTC TTT CAG AGA AGT GTC CCA GGA      609
140      Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
141      95 100 105
142
143
144      CAT GAT AAT AAG ATG CAA TTT GAA TCT TCA TCA TAC GAA GGA TAC TTT      657
145      His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
146      110 115 120
147      CTA GCT TGT GAA AAA GAG AGA GAC CTT TTT AAA CTC ATT TTG AAA AAA      705
148      Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
149      125 130 135 140
150      GAG GAT GAA TTG GGG GAT AGA TCT ATA ATG TTC ACT GTT CAA AAC GAA      753
151      Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
152      145 150 155

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RAW SEQUENCE LISTING  
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153 GAC TAGCTATTAA AATTTTCATGC CGGGCGCAGT GGCTCACGCC TGTAATCCCA 806  
154 Asp  
155 GCCCTTTGGG AGGCTGAGGC GGGCAGATCA CCAGAGGTCA GGTGTTCAAG ACCAGCCTGA 866  
156 CCAACATGGT GAAACCTCAT CTCTACTAAA AATACTAAAA ATTAGCTGAG TGTAGTGACG 926  
157 CATGCCCTCA ATCCCAGCTA CTCAAGAGGC TGAGGCAGGA GAATCACTTG CACTCCGGAG 986  
158 GTAGAGGTTG TGGTGAGCCG AGATTGCACC ATTGCGCTCT AGCCTGGGCA ACAACAGCAA 1046  
159 AACTCCATCT CAAAAAATAA AATAAATAA TAAACAAATA AAAAATTCAT AATGTGAAAA 1106  
160 AAAAAAAAAA AAAA 1120

161

162 (2) INFORMATION FOR SEQ ID NO: 3:

163

164 (i) SEQUENCE CHARACTERISTICS:

165 (A) LENGTH: 135 base pairs

166 (B) TYPE: nucleic acid

167 (C) STRANDEDNESS: double

168 (D) TOPOLOGY: linear

169

170 (ii) MOLECULE TYPE: Genomic DNA

171

172 (vi) ORIGINAL SOURCE:

173 (A) ORGANISM: human

174 (F) TISSUE TYPE: placenta

175

176 (ix) FEATURE:

177 (A) NAME/KEY: exon

178 (B) LOCATION: 1..135

179 (C) IDENTIFICATION METHOD: S

180

181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

182

183 AA AAC CTG GAA TCA GAT TAC TTT GGC AAG CTT GAA TCT AAA TTA TCA 47

184 Glu Asn Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser

185 -5 1 5 10

186 GTC ATA AGA AAT TTG AAT GAC CAA GTT CTC TTC ATT GAC CAA GGA AAT 95

187 Val Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn

188 15 20 25

189 CGG CCT CTA TTT GAA GAT ATG ACT GAT TCT GAC TGT AGA G 135

190 Arg Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp

191 30 35 40

192

193 (2) INFORMATION FOR SEQ ID NO: 4:

194

195 (i) SEQUENCE CHARACTERISTICS:

196 (A) LENGTH: 134 base pairs

197 (B) TYPE: nucleic acid

198 (C) STRANDEDNESS: double

199 (D) TOPOLOGY: linear

200

201 (ii) MOLECULE TYPE: Genomic DNA

202

203 (vi) ORIGINAL SOURCE:

204 (A) ORGANISM: human

205 (F) TISSUE TYPE: placenta

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206  
207 (ix) FEATURE:  
208 (A) NAME/KEY: exon  
209 (B) LOCATION: 1..134  
210 (C) IDENTIFICATION METHOD: S  
211  
212  
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
214  
215 AT AAT GCA CCC CGG ACC ATA TTT ATT ATA AGT ATG TAT AAA GAT AGC 47  
216 Asp Asn Ala Pro Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser  
217 40 45 50 55  
218 CAG CCT AGA GGT ATG GCT GTA ACT ATC TCT GTG AAG TGT GAG AAA ATT 95  
219 Gln Pro Arg Gly Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile  
220 60 65 70  
221 TCA ACT CTC TCC TGT GAG AAC AAA ATT ATT TCC TTT AAG 134  
222 Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys  
223 80 85  
224  
225 (2) INFORMATION FOR SEQ ID NO: 5:  
226  
227 (i) SEQUENCE CHARACTERISTICS:  
228 (A) LENGTH: 87 base pairs  
229 (B) TYPE: nucleic acid  
230 (C) STRANDEDNESS: double  
231 (D) TOPOLOGY: linear  
232  
233 (ii) MOLECULE TYPE: Genomic DNA  
234  
235 (vi) ORIGINAL SOURCE:  
236 (A) ORGANISM: human  
237 (F) TISSUE TYPE: placenta  
238  
239 (ix) FEATURE:  
240 (A) NAME/KEY: exon  
241 (B) LOCATION: 1..87  
242 (C) IDENTIFICATION METHOD: S  
243  
244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
245  
246 GAATAAAG ATG GCT GCT GAA CCA GTA GAA GAC AAT TGC ATC AAC TTT GTG 50  
247 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val  
248 -35 -30 -25  
249 GCA ATG AAA TTT ATT GAC AAT ACG CTT TAC TTT ATA G 87  
250 Ala Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala  
251 -20 -15 -10  
252  
253 (2) INFORMATION FOR SEQ ID NO:6:  
254  
255 (i) SEQUENCE CHARACTERISTICS:  
256 (A) LENGTH: 12 base pairs  
257 (B) TYPE: nucleic acid  
258 (C) STRANDEDNESS: double

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION *US/09/479,862*

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*INPUT SET: S36235.raw*

Line

Error

Original Text

PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/09/479,862**

DATE: 12/20/2000  
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*INPUT SET: S36235.raw*

< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/09/479,862DATE: 12/20/2000  
TIME: 22:21:00

INPUT SET: S36235.raw

Line	Original Text	Corrected Text
99	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
102	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
105	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
108	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
179	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
210	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
242	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
270	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
295	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
365	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
410	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
512	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
682	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
727	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
806	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
809	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
812	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
815	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
818	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
821	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
824	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
827	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
830	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
833	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
836	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
839	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
1088	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
1091	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
1094	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
1097	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
1100	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
1103	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
1106	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
1109	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
1112	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
1115	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
1118	(C) IDENTIFICATION METHODS: S	(C) IDENTIFICATION METHOD: S
1121	(C) IDENTIFICATION METHODS: E	(C) IDENTIFICATION METHOD: E
1646	(15) INFORMATION FOR SEQ ID NO: 15:	(2) INFORMATION FOR SEQ ID NO: 15: